SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Hilton, Douglas J.

    (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

   (iii) NUMBER OF SEQUENCES: 25

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
        (B) STREET: 400 Garden City Plaza
        (C) CITY: Garden City
        (D) STATE: New York
        (E) COUNTRY: United States of America
        (F) ZIP: 11530

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/702,665
        (B) FILING DATE: 20-DEC-1996
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:

        (A) NAME: Presser, Leopold
        (B) REGISTRATION NUMBER: 19,827
        (C) REFERENCE/DOCKET NUMBER: 10296

   (ix) TELECOMMUNICATION INFORMATION:

        (A) TELEPHONE: (516) 742-4343
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        (C) TELEX: 203 901 SANS UR

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 5 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 3..3
        (D) OTHER INFORMATION: /note= "Xaa at Position 3 is any amino acid"

1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Trp Ser Xaa Trp Ser
1               5
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1705 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:

        (A) NAME/KEY: CDS
        (B) LOCATION: 45..1340

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC        56
                                                 Met Ser Ser Ser
                                                  1

TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG        104
Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val
 5               10                  15                  20

TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG        152
Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln
                25                  30                  35

TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT        200
Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser
                40                  45                  50

GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC        248
Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu
                55                  60                  65

CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG        296
Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val
        70                  75                  80

GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA        344
Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val
85                  90                  95                  100

TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT        392
Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro
                105                 110                 115

GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG        440
Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp
                120                 125                 130
```

2

```
AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC        488
Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr
        135                     140                     145

AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC        536
Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser
        150                     155                     160

ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT        584
Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys
165                     170                     175                 180

GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC        632
Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr
                185                     190                     195

GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA        680
Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu
                200                     205                     210

CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC        728
Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser
                215                     220                     225

GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC        776
Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala
        230                     235                     240

TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC        824
Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr
245                     250                     255                 260

CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG        872
Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu
                265                     270                     275

GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA        920
Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg
                280                     285                     290

GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC        968
Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser
        295                     300                     305

CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA       1016
Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile
        310                     315                     320

CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT       1064
Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala
325                     330                     335                 340

CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA       1112
Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro
                345                     350                     355

AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG       1160
Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala
                360                     365                     370
```

3

```
TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA          1208
Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala
        375                 380                 385

CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA          1256
Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln
        390                 395                 400

AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA          1304
Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly
405                 410                 415                 420

ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTCATC              1350
Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
                425                 430

TGTAACCCGG TCAGACTGGG GGCAGAAAGA GGCGGGGCAG TGGATCCCTG TGGATGGAGG        1410

TCTCAGCTGA AAGTCTGAGC TCTTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT        1470

GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA        1530

AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT        1590

GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA        1650

GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAA            1705
```

(2) INFORMATION FOR SEQ ID NO:3:

      (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 432 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala
1               5                   10                  15

Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
            20                  25                  30

Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys
            35                  40                  45

Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp
        50                  55                  60

Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val
65                  70                  75                  80

Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr
                85                  90                  95
```

4

Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
                100   105   110

Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
        115   120   125

Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
    130   135   140

Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
145   150   155   160

Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
                165   170   175

Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
            180   185   190

Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
        195   200   205

Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
    210   215   220

Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp
225   230   235   240

Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe
                245   250   255

Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
                260   265   270

Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
            275   280   285

His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
    290   295   300

Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu
305   310   315   320

Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu
                325   330   335

Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu
            340   345   350

Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val
        355   360   365

Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val
    370   375   380

Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys
385   390   395   400

Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu
                405   410   415

5

```
Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
          420                   425                   430
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1800 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (ix) FEATURE:

        (A) NAME/KEY: CDS
        (B) LOCATION: 128..1396

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTTCTCC TAGGAAGCCT CAGTTTTGGA      60

GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTTGAC TCTACCTCTC     120

CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC      169
        Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala
          1               5                  10

GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG      217
Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp
 15                  20              25                  30

GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG      265
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu
              35                  40                  45

TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT      313
Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp
              50                  55                  60

GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA      361
Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu
              65                  70                  75

CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC      409
Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys
        80                  85                  90

CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC      457
Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly
 95                  100                 105                 110
```

6

```
TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG         505
Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu
                115                 120                 125

AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC         553
Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr
            130                 135                 140

CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT GAT AGC         601
Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser
        145                 150                 155

CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC         649
Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro
    160                 165                 170

CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG         697
Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln
175                 180                 185                 190

TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA         745
Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr
                195                 200                 205

CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC         793
Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro
            210                 215                 220

CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA         841
Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg
        225                 230                 235

GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG         889
Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu
        240                 245                 250

CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC         937
Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser
255                 260                 265                 270

ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT         985
Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala
            275                 280                 285

GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT        1033
Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala
            290                 295                 300

GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT        1081
Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr
            305                 310                 315

GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG        1129
Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln
        320                 325                 330

CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC        1177
Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser
```

7

```
CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG    1225
Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln
            355             360                 365

GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG GTG    1273
Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val
            370             375                 380

GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG    1321
Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly
            385             390                 395

AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG    1369
Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val
            400             405                 410

GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT         1416
Asp Arg Arg Pro Gly Ala Pro Asn Leu
415                 420

CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA    1476

GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGGA GCCCATTTCT GTGAGACCCT    1536

GTATTTCAAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTCACCCCA GAGTTGGAGT    1596

TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG    1656

AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG    1716

TCCTTGGCTC TTGGCCTTTC CCCTTGCAGG GGTTGTGCAG GTGTGAATAA AGAGAATAAG    1776

GAAGTTCTTG GAGATTATAC TCAG                                          1800
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 423 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
1               5                   10                  15

Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
            20              25                  30

Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys
            35              40                  45

Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu
```

```
        50                    55                    60

Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val
 65                  70                  75                  80

Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr
                 85                  90                  95

Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro
            100                 105                 110

Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
            115                 120                 125

Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
        130                 135                 140

Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
145                 150                 155                 160

Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
            165                 170                 175

Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
            180                 185                 190

Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr Arg Leu
        195                 200                 205

Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly
    210                 215                 220

Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser
225                 230                 235                 240

Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys
            245                 250                 255

Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val
            260                 265                 270

Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu
            275                 280                 285

Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr
    290                 295                 300

Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr
305                 310                 315                 320

Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu
            325                 330                 335

Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln
            340                 345                 350

Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala
        355                 360                 365
```

9

```
Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly
    370                 375                 380

Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp
385                 390                 395                 400

Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg
                405                 410                 415

Arg Pro Gly Ala Pro Asn Leu
            420
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1..2
        (D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 7..8
        (D) OTHER INFORMATION: /note= "Y at Position 7 is C or T"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 10..11
        (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
RCTCCAYTCR CTCCA                                                15
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 7..8
        (D) OTHER INFORMATION: /note= "R at Position 7 is A or G"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 10..11
        (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

RCTCCARTCR CTCCA   15

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1..2
        (D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 7..8
        (D) OTHER INFORMATION: /note= "N at Position 7 is N"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 10..11
        (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

RCTCCANGCR CTCCA   15

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..2
    (D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 7..8
    (D) OTHER INFORMATION: /note= "N at Position 7 is N"

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 10..11
    (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

RCTCCANGGR CTCCA   15

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..2
    (D) OTHER INFORMATION: /note= "R at Position 1 is A or G"

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 7..8
    (D) OTHER INFORMATION: /note= "Y at Position 7 is C or T"

(ix) FEATURE:

    (A) NAME/KEY: misc_feature
    (B) LOCATION: 10..11
    (D) OTHER INFORMATION: /note= "R at Position 10 is A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RCTCCAYTTR CTCCA   15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTCCACGG TGGAGCCCAT TGGCT   25

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCACACGCGG TACGAGTCAG TGCCAGGGAC   30

(2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 21 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAAGTTCA GCCTGGTTAA G   21

(2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTATGAGTA TTTCTTCCAG GGTA   24

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCTTCATTG ACCTCAACTA CATG   24

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGCCAGTG AGCTTCCCGT TCAG   24

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTCCTCCA GGGGTCCAGT ATGG   24

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGGCCTCC AGAGGGT   17

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCCTGTACT TGGAGTCCAG G   21

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAAAGCTGT GGCGTGATGG CCGTGGGGCA   30

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCGGAGGC CGCTGGCGGG CG   22

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTATCAGCTG AAGTTCTCTG GGG   23

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1..2
        (D) OTHER INFORMATION: /note= "R at Position 1 is G or A"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 7..8
        (D) OTHER INFORMATION: /note= "N at Position 7 is N"

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature
        (B) LOCATION: 10..11
        (D) OTHER INFORMATION: /note= "R at Position 10 is G or A"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

RCTCCANGCR CTCAA   15

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 28 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCTTCTAGA TCCCCCTGCC CCCAAGCT   28

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACTTTCTAGA TTATTGCTCC AAGGGGTCCC TGTG   34